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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/612,809B

DATE: 02/10/2003

TIME: 15:04:09

Input Set : A:\Iowa042.app

Output Set : N:\CRF4\02102003\I612809B.raw

3 <110> APPLICANT: SHEFFIELD, VAL C.
 4 AIWARI, WALLACE L.M.
 5 STONE, EDWIN M.
 6 HUSHIMURA, DARRYL
 7 PATIL, SHIVA
 9 <120> TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR CONGENITAL HEART
 10 DISEASE BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
 12 <130> FILE REFERENCE: IOWA:042USD1
 14 <140> CURRENT APPLICATION NUMBER: 09/612,809B
 15 <141> CURRENT FILING DATE: 2000-07-10
 17 <160> NUMBER OF SEQ ID NOS: 20
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <110> SEQ ID NO: 1
 22 <111> LENGTH: 2284
 23 <112> TYPE: DNA
 24 <113> ORGANISM: Homo sapiens
 26 <114> SEQUENCE: 1

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19 agtgggga ggc ggcggggggg ggtctctctt cctttctctt cgtctctctt cgtctctctt 180
20 cgtgggaggc cgcgggggagg ggtctctctt cgtctctctt cgtctctctt cgtctctctt 240
21 cgtgggaggc ggcggggggg cgcgggggagg cgcgggggagg ggtctctctt cgtctctctt 300
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52 ctgtgggggc agatatgcac agataaatat ttggcttggtg tattccatat aaaatigcag 1620
54 tgratattat aacacccigt gagccagatg ctgaatagat ttttccat tattccagtc 1680
56 ctttataaaa ggaataataa accagttttt aaatgtatgt atataattct ccccattht 1740
58 caatccctca tgtattacat agaaggattg cttttttaaa aatatactgc ggggttgaaa 1800
60 gggatattta atctttgaga aactatttta gaaaatatgt ttgtagaaca attatttttg 1860
62 aaaaagattt aaagaaataa caagaaggaa ggcgagagga gcagaacatt ttggtctagg 1920
64 gtggtttctt tttaaaccat tttttcttgt taatttacag ttaaacctag gggacaatcc 1980
66 ggahtggccc tccctctttt gtaataaacc caggaaatgt aataaattca ttatcttagg 2040
68 gttttctgac ctgcaaatca gactttgggg agatggcgat ttgattacag acgttcgggg 2100
70 ggttgggggg cttgcagttt gttttggaga taatacagtt tctgtctatc tgggtctat 2160
72 atctagaggg aacatttaag cagtaattgc tgttgattgt tgtcaaat ttgatattgt 2220
74 aaaggattg ctgcaataa atacacttta atttcagtc aaaaaaaaaa aaaaaaaaaa 2280
76 aaaa
78 010 - SEQ ID NO: 2
79 011 - LENGTH: 553
80 012 - TYPE: PRO
81 013 - ORGANISM: Homo sapiens
82 010 - SEQUENCE: 2
83 Met Gln Ala Arg Tyr Ser Val Ser Ser Pro Asn Ser Leu Gly Val Val
84 1 5 10 15
85 Pro Tyr Leu Gly Gln Gln Ser Tyr Tyr Arg Ala Ala Ala Ala Ala
86 20 25 30
87 Ala Gly Gly Tyr Thr Ala Met Pro Ala Pro Met Ser Val Tyr Ser
88 35 40 45
89 His Pro Ala His Ala Glu Gln Tyr Pro Gly Gly Met Ala Arg Ala Tyr
90 50 55 60
91 Gly Pro Tyr Thr Pro Gln Pro Gln Pro Lys Asp Met Val Lys Pro Pro
92 65 70 75 80
93 Tyr Ser Tyr Ile Ala Leu Ile Thr Met Ala Ile Gln Asn Ala Pro Asp
94 85 90 95
95 Lys Lys Ile Thr Leu Asn Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe
96 100 105 110
97 Pro Phe Tyr Arg Asp Asn Lys Gln Gly Trp Gln Asn Ser Ile Arg His
98 115 120 125
99 Asn Leu Ser Leu Asn Glu Cys Phe Val Lys Val Pro Arg Asp Asp Lys
100 130 135 140
101 Lys Pro Gly Lys Gly Ser Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asn
102 145 150 155 160
103 Met Phe Glu Asn Gly Ser Phe Leu Arg Arg Arg Arg Arg Phe Lys Lys
104 165 170 175
105 Lys Asp Ala Val Lys Asp Lys Glu Glu Lys Asp Arg Leu His Leu Lys
106 180 185 190
107 Glu Pro Pro Pro Pro Gly Arg Gln Pro Pro Pro Ala Pro Pro Glu Gln
108 195 200 205
109 Ala Asp Gly Asn Ala Pro Gly Pro Gln Pro Pro Pro Val Arg Ile Gln
110 210 215 220
111 Asp Ile Lys Thr Glu Asn Gly Thr Cys Pro Ser Pro Pro Gln Pro Leu
112 225 230 235 240
113 Ser Pro Ala Ala Ala Leu Gly Ser Gly Ser Ala Ala Val Pro Lys

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120                               245                               250                               155
122 Ile Glu Ser Pro Asp Ser Ser Ser Ser Ser Leu Ser Ser Gly Ser Ser
123                               260                               265                               170
125 Pro Pro Gly Ser Leu Pro Ser Ala Arg Pro Leu Ser Leu Asp Gly Ala
126                               275                               280                               285
128 Asp Ser Ala Pro Pro Pro Pro Ala Pro Ser Ala Pro Pro Pro His His
129                               290                               295                               300
131 Ser Gln Gly Phe Ser Val Asp Asn Ile Met Thr Ser Leu Arg Gly Ser
132                               305                               310                               315
134 Pro Gln Ser Ala Ala Ala Glu Leu Ser Ser Gly Leu Leu Ala Ser Ala
135                               320                               325                               330
137 Ala Ala Ser Ser Arg Ala Gly Ile Ala Pro Pro Leu Ala Leu Gly Ala
138                               335                               340                               345
139 Tyr Ser Pro Gly Gln Ser Ser Leu Tyr Ser Ser Pro Cys Ser Gln Thr
140                               350                               355                               360
142 Ser Ser Ala Gly Ser Ser Gly Gly Gly Gly Gly Gly Ala Gly Ala Ala
143                               365                               370                               375
145 Gly Gly Ala Gly Gly Ala Gly Thr Tyr His Cys Asn Leu Glu Ala Met
146                               380                               385                               390
148 Ser Leu Tyr Ala Ala Gly Glu Arg Gly Gly His Leu Gln Gly Ala Pro
149                               395                               400                               405
151 Gly Gly Ala Gly Gly Ser Ala Val Asp Asn Pro Leu Pro Asp Tyr Ser
152                               410                               415                               420
154 Leu Pro Pro Val Thr Ser Ser Ser Ser Ser Ser Ser Leu Ser His Gly Gly
155                               425                               430                               435
157 Gly Gly Gly Gly Gly Gly Gly Gly Gln Glu Ala Gly His His Pro Ala
158                               440                               445                               450
160 Ala His Gln Gly Arg Leu Thr Ser Trp Tyr Leu Asn Gln Ala Gly Gly
161                               455                               460                               465
163 Asp Leu Gly His Leu Ala Ser Ala Ala Ala Ala Ala Ala Ala Gly
164                               470                               475                               480
166 Tyr Pro Gly Gln Gln Gln Asn Phe His Ser Val Arg Glu Met Phe Glu
167                               485                               490                               495
169 Ser Gln Arg Ile Gly Leu Asn Asn Ser Pro Val Asn Gly Asn Ser Ser
170                               500                               505                               510
172                               515                               520                               525
174 Cys Gln Met Ala Phe Pro Ser Ser Gln Ser Leu Tyr Arg Thr Ser Gly
175                               530                               535                               540
176 Ala Phe Val Tyr Asp Cys Ser Lys Phe
177 545                               550
180 <Q10> SEQ ID NO: 3
181 <Q11> LENGTH: 1662
182 <Q12> TYPE: DNA
183 <Q13> ORGANISM: Homo sapiens
184 <Q14> SEQUENCE: 3
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187 ggagggagag gctactccgc cggggcgggc gggcgccc ggagggcta cactggcatg 120
188 cgggccccca ttagcgtgta ctgcacccct jcgtagccag agagtagccc gggaggcatg 180
189 gcccgccgct acggggccca cagcccgag ccgagccca aggagatggt gaaagccccc 240
190 tatactaca tggggtcat caccatggcc atccagaacj cccgggacaa gaagatcacc 300

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191 ctgaacgggca tctaacagtt catcatagag cgtttccctt tctaacgggta caa-aagagag 360
192 gctgggagaa atagatcttg ccacaaactc tggctcaacg agtgccttct caa-ggagccg 420
193 ctggagacaa agaaacgggg caagggagag taatggacgc tggacccgga ctccacaaac 480
194 atgtttcaga atggatgctt cctggcgagg cggcgagcgt tcaagaagaa ggaacgggtg 540
195 atggagaaag aggaagagga cagctcgac ctcaagggag cgcacccgac cggcggagag 600
196 ccccgagcag cggcgagaga gcaaggcgac gcaaacgggc cgggtccgta ggcggcgccc 660
197 atggccttcc aggaatctta gacgagaa agtaactgca cctggcgac ccagacccctg 720
198 tcccgaggag cggccctggg caggggagag ggcggcgagg tgcacaaagt cgaagagccc 780
199 atagcagaga ggaagagcct gtccagggg agcagacccc cggagagcct ggcgtggggg 840
200 atggcgctta gctggaggg tgggattcc ggcagagcgc cgcagcgac ctccggcccg 900
201 cggcgcaaac atagagaggg attcagcgag gacaaatcca tgactgcctt gggggggctg 960
202 atggagagag cggcgaggga gctcagctcc ggccttatgg cctggcgac cgggtccctg 1020
203 cggcgaggga tggcaccccc gctggcgctc ggagctact cgcacggcga gactccctc 1080
204 atgacccccc cctgagagca gacctcagc ggggagagct cggcgaggag cggcgaggag 1140
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208 atgtgctccc tggcaccgg cggcgaggag gggcgaggag gggcgaggag gggcgaggag 1380
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210 atctgggggc atttgcaag cggcgaggag gggcgaggag cgcagagcta cccggggcag 1500
211 atgcagaaat tccactcgtt gggggagatg ttccagtcac agaggatcgg cttgaacaaac 1560
212 tctccagtaa atgggaatag tagctgtcaa atggccttcc cttccagata gtctatgtac 1620
213 ataacgtc-g gacatttcgt ctacgactgt agcaagtttt ga 1682

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110> SEQ ID NO: 4

111> LENGTH: 106

112> TYPE: PRT

113> ORGANISM: Artificial Sequence

114> FEATURE:

115> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

116> Feature

117> SEQUENCE: 4

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118> 1 Lys Asp Met Val Lys Pro Pro Tyr Ser Tyr Ile Ala Leu Ile Thr
119> 5 10 15
120> 20 Met Ala Ile Gln Asn Ala Pro Asp Lys Lys Ile Thr Leu Asn Gly Ile
121> 25 30
122> 35 Tyr Gln Phe Ile Met Asp Arg Phe Pro Phe Tyr Arg Asp Asn Lys Gln
123> 40 45
124> 50 Gly Trp Gln Asn Ser Ile Arg His Asn Leu Ser Leu Asn Glu Cys Phe
125> 55 60
126> 65 Lys Val Pro Arg Asp Asp Lys Lys Pro Gly Lys Gly Ser Tyr Trp
127> 70 75 80
128> 85 Thr Leu Asp Pro Asp Ser Tyr Asn Met Phe Glu Asn Gly Ser Phe Leu
129> 90 95
130> 100 Arg Arg Arg Arg Arg Phe Lys Lys Lys Asp
131> 105 110

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110> SEQ ID NO: 5

111> LENGTH: 106

112> TYPE: PRT

113> ORGANISM: Artificial Sequence

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253 <220> FEATURE:

254 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

255 Peptide

257 <410> SEQUENCE: 5

258 Thr Lys Asp Leu Val Lys Pro Pro Tyr Ser Tyr Ile Ala Leu Ile Thr

259 1 5 10 15

260 Met Ala Ile Gln Asn Ala Pro Glu Lys Lys Ile Thr Leu Asn Gly Ile

261 20 30

262 Tyr Gln Phe Ile Met Asp Arg Phe Pro Phe Tyr Arg Glu Asn Lys Gln

263 35 40 45

264 Gly Trp Gln Asn Ser Ile Arg His Asn Leu Ser Leu Asn Glu Cys Phe

265 50 55 60

266 Val Lys Val Pro Arg Asp Asp Lys Lys Pro Gly Lys Gly Ser Tyr Trp

267 65 70 75 80

268 Thr Leu Asp Pro Asp Ser Tyr Asn Met Phe Glu Asn Gly Ser Phe Leu

269 85 90 95

270 Arg Arg Arg Arg Arg Phe Lys Lys Lys Asp

271 100 105

272 <410> SEQ ID NO: 6

273 <411> LENGTH: 106

274 <412> TYPE: PPT

275 <413> ORGANISM: Artificial Sequence

276 <410> FEATURE:

277 <413> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

278 Peptide

280 <410> SEQUENCE: 5

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282 1 5 10 15

283 Met Ala Ile Gln Ser Ser Pro Gly Gln Arg Ala Thr Leu Ser Gly Ile

284 20 30

285 Tyr Arg Val Ile Met Gly Arg Phe Ala Phe Tyr Arg His Asn Arg Pro

286 35 40 45

287 Gly Trp Gln Asn Ser Ile Arg His Asn Leu Ser Leu Asn Glu Cys Phe

288 50 55 60

289 Val Lys Val Pro Arg Asp Asp Arg Lys Pro Gly Lys Gly Ser Tyr Trp

290 65 70 75 80

291 Thr Leu Asp Pro Asp Cys His Asp Met Phe Glu His Gly Ser Phe Leu

292 85 90 95

293 Arg Arg Arg Arg Arg Phe Thr Arg Gln Thr

294 100 105

295 <410> SEQ ID NO: 7

296 <411> LENGTH: 106

297 <412> TYPE: PPT

298 <413> ORGANISM: Artificial Sequence

299 <410> FEATURE:

300 <413> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

301 Peptide

302 <410> SEQUENCE: 7

303 Ala Glu Thr Pro Gln Lys Pro Pro Tyr Ser Tyr Ile Ala Leu Ile Ala

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